

SEQUENCE LISTING

#5/a

FEB 25 1999

GROUP 1800



(1) GENERAL INFORMATION

(i) APPLICANT: Hillman, Jennifer L.
 Lal, Preeti
 Tang, Y. Tom
 Yue, Henry
 Corley, Neil C.

(ii) TITLE OF THE INVENTION: KINESIN LIGHT CHAIN HOMOLOG

(iii) NUMBER OF SEQUENCES: 3

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: Incyte Pharmaceuticals, Inc.
 (B) STREET: 3174 Porter Dr.
 (C) CITY: Palo Alto
 (D) STATE: CA
 (E) COUNTRY: USA
 (F) ZIP: 94304

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Diskette
 (B) COMPUTER: IBM Compatible
 (C) OPERATING SYSTEM: DOS
 (D) SOFTWARE: FastSEQ for Windows Version 2.0

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: To Be Assigned
 (B) FILING DATE: Filed Herewith

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER:
 (B) FILING DATE:

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Billings, Lucy J.
 (B) REGISTRATION NUMBER: 36,749
 (C) REFERENCE/DOCKET NUMBER: PF-0484 US

(ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: 650-855-0555
 (B) TELEFAX: 650-845-4166

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 619 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

(A) LIBRARY: SMCANOT01
 (B) CLONE: 2479739

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

Met	Ser	Gly	Leu	Val	Leu	Gly	Gln	Arg	Asp	Glu	Pro	Ala	Gly	His	Arg
1				5					10					15	
Leu	Ser	Gln	Glu	Glu	Ile	Leu	Gly	Ser	Thr	Arg	Leu	Val	Ser	Gln	Gly
			20					25					30		
Leu	Glu	Ala	Leu	Arg	Ser	Glu	His	Gln	Ala	Val	Leu	Gln	Ser	Leu	Ser
		35					40					45			
Gln	Thr	Ile	Glu	Cys	Leu	Gln	Gln	Gly	Gly	His	Glu	Glu	Gly	Leu	Val
50						55						60			

His	Glu	Lys	Ala	Arg	Gln	Leu	Arg	Arg	Ser	Met	Glu	Asn	Ile	Glu	Leu
65					70					75					80
Gly	Leu	Ser	Glu	Ala	Gln	Val	Met	Leu	Ala	Leu	Ala	Ser	His	Leu	Ser
				85					90					95	
Thr	Val	Glu	Ser	Glu	Lys	Gln	Lys	Leu	Arg	Ala	Gln	Val	Arg	Arg	Leu
			100					105					110		
Cys	Gln	Glu	Asn	Gln	Trp	Leu	Arg	Asp	Glu	Leu	Ala	Gly	Thr	Gln	Gln
		115					120					125			
Arg	Leu	Gln	Arg	Ser	Glu	Gln	Ala	Val	Ala	Gln	Leu	Glu	Glu	Glu	Lys
	130					135					140				
Lys	His	Leu	Glu	Phe	Leu	Gly	Gln	Leu	Arg	Gln	Tyr	Asp	Glu	Asp	Gly
145				150					155						160
His	Thr	Ser	Glu	Glu	Lys	Glu	Gly	Asp	Ala	Thr	Lys	Asp	Ser	Leu	Asp
				165					170					175	
Asp	Leu	Phe	Pro	Asn	Glu	Glu	Glu	Glu	Asp	Pro	Ser	Asn	Gly	Leu	Ser
		180						185					190		
Arg	Gly	Gln	Gly	Ala	Thr	Ala	Ala	Gln	Gln	Gly	Gly	Tyr	Glu	Ile	Pro
		195					200					205			
Ala	Arg	Leu	Arg	Thr	Leu	His	Asn	Leu	Val	Ile	Gln	Tyr	Ala	Ala	Gln
	210					215					220				
Gly	Arg	Tyr	Glu	Val	Ala	Val	Pro	Leu	Cys	Lys	Gln	Ala	Leu	Glu	Asp
225				230						235					240
Leu	Glu	Arg	Thr	Ser	Gly	Arg	Gly	His	Pro	Asp	Val	Ala	Thr	Met	Leu
				245					250					255	
Asn	Ile	Leu	Ala	Leu	Val	Tyr	Arg	Asp	Gln	Asn	Lys	Tyr	Lys	Glu	Ala
			260					265					270		
Ala	His	Leu	Leu	Asn	Asp	Ala	Leu	Ser	Ile	Arg	Glu	Ser	Thr	Leu	Gly
	275						280					285			
Pro	Asp	His	Pro	Ala	Val	Ala	Ala	Thr	Leu	Asn	Asn	Leu	Ala	Val	Leu
	290					295					300				
Tyr	Gly	Lys	Arg	Gly	Lys	Tyr	Lys	Glu	Ala	Glu	Pro	Leu	Cys	Gln	Arg
305				310						315					320
Ala	Leu	Glu	Ile	Arg	Glu	Lys	Val	Leu	Gly	Thr	Asn	His	Pro	Asp	Val
				325					330					335	
Ala	Lys	Gln	Leu	Asn	Asn	Leu	Ala	Leu	Leu	Cys	Gln	Asn	Gln	Gly	Lys
			340					345					350		
Tyr	Glu	Ala	Val	Glu	Arg	Tyr	Tyr	Gln	Arg	Ala	Leu	Ala	Ile	Tyr	Glu
	355						360					365			
Gly	Gln	Leu	Gly	Pro	Asp	Asn	Pro	Asn	Val	Ala	Arg	Thr	Lys	Asn	Asn
	370					375					380				
Leu	Ala	Ser	Cys	Tyr	Leu	Lys	Gln	Gly	Lys	Tyr	Ala	Glu	Ala	Glu	Thr
385				390						395					400
Leu	Tyr	Lys	Glu	Ile	Leu	Thr	Arg	Ala	His	Val	Gln	Glu	Phe	Gly	Ser
				405					410					415	
Val	Asp	Asp	Asp	His	Lys	Pro	Ile	Trp	Met	His	Ala	Glu	Glu	Arg	Glu
			420					425					430		
Glu	Met	Ser	Lys	Ser	Arg	His	His	Glu	Gly	Gly	Thr	Pro	Tyr	Ala	Glu
		435					440					445			
Tyr	Gly	Gly	Trp	Tyr	Lys	Ala	Cys	Lys	Val	Ser	Ser	Pro	Thr	Val	Asn
	450				455						460				
Thr	Thr	Leu	Arg	Asn	Leu	Gly	Ala	Leu	Tyr	Arg	Arg	Gln	Gly	Lys	Leu
465				470						475					480
Glu	Ala	Ala	Glu	Thr	Leu	Glu	Glu	Cys	Ala	Leu	Arg	Ser	Arg	Arg	Gln
				485					490					495	
Gly	Thr	Asp	Pro	Ile	Ser	Gln	Thr	Lys	Val	Ala	Glu	Leu	Leu	Gly	Glu
			500					505					510		
Ser	Asp	Gly	Arg	Arg	Thr	Ser	Gln	Glu	Gly	Pro	Gly	Asp	Ser	Val	Lys
		515					520					525			
Phe	Glu	Gly	Gly	Glu	Asp	Ala	Ser	Val	Ala	Val	Glu	Trp	Ser	Gly	Asp
	530					535					540				
Gly	Ser	Gly	Thr	Leu	Gln	Arg	Ser	Gly	Ser	Leu	Gly	Lys	Ile	Arg	Asp
545				550						555					560
Val	Leu	Arg	Arg	Ser	Ser	Glu	Leu	Leu	Val	Arg	Lys	Leu	Gln	Gly	Thr
				565					570					575	
Glu	Pro	Arg	Pro	Ser	Ser	Ser	Asn	Met	Lys	Arg	Ala	Ala	Ser	Leu	Asn
			580					585					590		
Tyr	Leu	Asn	Gln	Pro	Ser	Ala	Ala	Pro	Leu	Gln	Val	Ser	Arg	Gly	Leu

595 600 605
 Ser Ala Ser Thr Met Asp Leu Ser Ser Ser Ser
 610 615

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2453 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: SMCANOT01
 (B) CLONE: 2479739

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

GTGAAGTGGT	GAAAGAAGGG	GTGGGAACGC	TGGACTTCTG	GACTTTGGGC	AGGGCAGATC	60
CTCTGACTCT	CTGGCTGCAG	AACAGTTTCT	TCCGTGCTCT	GGCCTGAGTG	CCCACAGGCC	120
AGGGGCCTCT	GCTCTGTACA	CAGACCGGGC	AAGGTCCCCC	AGGCCAGGAT	GTCAGGCCTG	180
GTGTTGGGGC	AGCGGGATGA	GCCTGCAGGC	CACCGGCTCA	GCCAAGAGGA	GATCCTGGGG	240
AGCACACGGC	TGGTCAGCCA	AGGGCTAGAG	GCCCTACGCA	GTGAACACCA	GGCCGTGCTG	300
CAAAGCCTGT	CCCAGACCAT	TGAGTGTCTG	CAGCAGGGAG	GCCATGAGGA	AGGGCTGGTG	360
CATGAGAAGG	CCCGGCAGCT	TCGCCGTTCT	ATGGAAAACA	TTGAGCTCGG	GCTGAGTGAG	420
GCCCAGGTGA	TGCTGGCTCT	AGCCAGCCAC	CTGAGCACAG	TGGAGTCGGA	GAAACAGAAG	480
CTGCGGGCTC	AGGTGCGGCG	GCTATGCCAG	GAGAACCAGT	GGCTGCGGGA	TGAGCTGGCT	540
GGCACCCAGC	AGCGGCTACA	GCGCAGTGAA	CAGGCTGTGG	CTCAGCTGGA	GGAGGAAAAG	600
AAGCACCTGG	AGTTCCTGGG	GCAGCTGCGG	CAGTATGATG	AGGATGGACA	TACCTCGGAG	660
GAGAAAGAAG	GCGATGCCAC	CAAGGATTCC	CTGGATGACC	TCTTTCCTAA	TGAGGAGGAA	720
GAGGACCCCA	GCAATGGCTT	GTCCCGTGGT	CAAGGTGCTA	CAGCAGCTCA	GCAGGGTGGA	780
TATGAGATCC	CAGCAAGGTT	GCGGACGTTG	CACAACCTGG	TGATCCAGTA	CGCAGCCCAA	840
GGTCGCTATG	AGGTGGCCGT	GCCACTCTGT	AAGCAGGCAC	TAGAGGACCT	GGAGCGCACA	900
TCAGGCCGTG	GCCACCCTGA	TGTCGCCACC	ATGCTCAACA	TCCTTGCTTT	GGTGTATCGT	960
GACCAGAATA	AGTATAAGGA	AGCTGCCAC	CTGCTGAATG	ATGCCCTTAG	CATCCGGGAG	1020
AGCACCTTGG	GACCTGACCA	TCCTGCTGTG	GCTGCCACAC	TCAACAATT	GGCTGTGCTC	1080
TATGGCAAAA	GGGGCAAGTA	CAAGGAGGCA	GAGCCTCTGT	GCCAGCGGGC	ACTGGAGATT	1140
CGAGAAAAGG	TCCTGGGCAC	GAATCATCCA	GATGTGGCAA	AACAGCTGAA	CAACCTGGCC	1200
CTCTTGTGCC	AAAACCAGGG	CAAGTATGAG	GCCGTGGAAC	GCTACTACCA	GCGAGCACTG	1260
GCCATCTACG	AGGGGCAGCT	GGGGCCGGAC	AACCCTAATG	TAGCCCGGAC	CAAGAACAAC	1320
CTGGCTTCCT	GTTACCTGAA	ACAGGGCAAA	TATGCTGAGG	CTGAGACACT	ATACAAAGAG	1380
ATCCTGACCC	GTGCCCATGT	ACAGGAGTTT	GGGTCTGTGG	ATGATGACCA	CAAGCCCATC	1440
TGGATGCATG	CAGAGGAGCG	GGAGGAAATG	AGCAAAAGCC	GGCACCATGA	GGGTGGGACA	1500
CCCTATGCTG	AGTATGGAGG	CTGGTACAAG	GCCTGCAAAG	TGAGCAGCCC	CACAGTGAAC	1560
ACTACTCTGA	GAAACCTGGG	AGCTCTGTAT	AGGCGCCAGG	GAAAGCTGGA	GGCTGCTGAG	1620
ACCCTGGAGG	AATGTGCCCT	GCGGTCCCCG	AGACAGGGCA	CTGACCCTAT	CAGCCAGACG	1680
AAGGTGGCAG	AGCTGCTTGG	GGAGAGTGAT	GGTAGAAGGA	CCTCCCAGGA	GGGCCCTGGA	1740
GACAGTGTGA	AATTCGAGGG	TGGTGAAGAT	GCTTCTGTGG	CTGTGGAGTG	GTCCGGGGAT	1800
GGCAGTGGGA	CCCTGCAGAG	GAGTGGCTCT	CTTGGCAAGA	TCCGGGATGT	GCTCCGCAGA	1860
AGCAGTGAAC	TCTTGGTGAG	GAAGCTCCAG	GGGACTGAGC	CTCGGCCCTC	CAGCAGCAAC	1920
ATGAAGCGAG	CAGCCTCCTT	GAACATCTTG	AACCAACCTA	GTGCAGCACC	CCTCCAGGTC	1980
TCCCCGGGGC	TCAGTGCCAG	CACCATGGAG	CTCTCTTCAA	GCAGCTGACA	TTCAACCCGG	2040
CCCCCAGGTC	TGCTG66T66	6666AG6666	ACAGCCCTCA	CAGCATTCCC	CATTGCTCCT	2100
GGCTCTTCCC	CACCCCTAGG	TGGGACAGTG	AAGGGGAGCA	GTTTAACCAG	AAGATTGCTG	2160
CTGCCCTTAG	GGTCTCAGCT	CCCTCCTCAG	GAATCCCTCT	TAGGAAGGAC	CCTCAGGACA	2220
CCCTCTCTGC	ACCCTGTGGT	CCTCTAGAGT	AGCTAGCTCT	GAGGCCCCAA	GGTGGGTACA	2280
AAGCAGGTAT	GGCCCTCAGA	GATGCAGCCT	GCTGCTGGCT	TTTCAGTCAG	AGGGTTGGGG	2340
GCTGGCCAGC	CAAGCTGCCT	TGCCCTGGCC	GCTCTTACTC	CCTCCCTCTG	CTGTCTCACT	2400
TCAGGTCCAT	GTATTTCACT	TTTCTTAAAT	AAAAGAATCA	GTNCTTNTNT	NNG	2453

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 569 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

(A) LIBRARY: GenBank

(B) CLONE: 307085

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

Met	Ser	Thr	Met	Val	Tyr	Ile	Lys	Glu	Asp	Lys	Leu	Glu	Lys	Leu	Thr
1				5					10					15	
Gln	Asp	Glu	Ile	Ile	Ser	Lys	Thr	Lys	Gln	Val	Ile	Gln	Gly	Leu	Glu
			20					25					30		
Ala	Leu	Lys	Asn	Glu	His	Asn	Ser	Ile	Leu	Gln	Ser	Leu	Leu	Glu	Thr
		35					40					45			
Leu	Lys	Cys	Leu	Lys	Lys	Asp	Asp	Glu	Ser	Asn	Leu	Val	Glu	Glu	Lys
	50					55					60				
Ser	Asn	Met	Ile	Arg	Lys	Ser	Leu	Glu	Met	Leu	Glu	Leu	Gly	Leu	Ser
65					70					75					80
Glu	Ala	Gln	Val	Met	Met	Ala	Leu	Ser	Asn	His	Leu	Asn	Ala	Val	Glu
				85					90					95	
Ser	Glu	Lys	Gln	Lys	Leu	Arg	Ala	Gln	Val	Arg	Arg	Leu	Cys	Gln	Glu
			100					105					110		
Asn	Gln	Trp	Leu	Arg	Asp	Glu	Leu	Ala	Asn	Thr	Gln	Gln	Lys	Leu	Gln
		115				120						125			
Lys	Ser	Glu	Gln	Ser	Val	Ala	Gln	Leu	Glu	Glu	Glu	Lys	Lys	His	Leu
	130					135					140				
Glu	Phe	Met	Asn	Gln	Leu	Lys	Lys	Tyr	Asp	Asp	Asp	Ile	Ser	Pro	Ser
145					150				155						160
Glu	Asp	Lys	Asp	Thr	Asp	Ser	Thr	Lys	Glu	Pro	Leu	Asp	Asp	Leu	Phe
			165						170					175	
Pro	Asn	Asp	Glu	Asp	Asp	Pro	Gly	Gln	Gly	Ile	Gln	Gln	Gln	His	Ser
			180					185					190		
Ser	Ala	Ala	Ala	Ala	Ala	Gln	Gln	Gly	Gly	Tyr	Glu	Ile	Pro	Ala	Arg
		195				200						205			
Leu	Arg	Thr	Leu	His	Asn	Leu	Val	Ile	Gln	Tyr	Ala	Ser	Gln	Gly	Arg
	210				215						220				
Tyr	Glu	Val	Ala	Val	Pro	Leu	Cys	Lys	Gln	Ala	Leu	Glu	Asp	Leu	Glu
225					230					235					240
Lys	Thr	Ser	Gly	His	Asp	His	Pro	Asp	Val	Ala	Thr	Met	Leu	Asn	Ile
			245						250				255		
Leu	Ala	Leu	Val	Tyr	Arg	Asp	Gln	Asn	Lys	Tyr	Lys	Asp	Ala	Ala	Asn
			260					265					270		
Leu	Leu	Asn	Asp	Ala	Leu	Ala	Ile	Arg	Glu	Lys	Thr	Leu	Gly	Lys	Asp
		275					280					285			
His	Pro	Ala	Val	Ala	Ala	Thr	Leu	Asn	Asn	Leu	Ala	Val	Leu	Tyr	Gly
	290					295					300				
Lys	Arg	Gly	Lys	Tyr	Lys	Glu	Ala	Glu	Pro	Leu	Cys	Lys	Arg	Ala	Leu
305					310					315					320
Glu	Ile	Arg	Glu	Lys	Val	Leu	Gly	Lys	Asp	His	Pro	Asp	Val	Ala	Lys
			325						330					335	
Gln	Leu	Asn	Asn	Leu	Ala	Leu	Leu	Cys	Gln	Asn	Gln	Gly	Lys	Tyr	Glu
			340					345					350		
Glu	Val	Glu	Tyr	Tyr	Tyr	Gln	Arg	Ala	Leu	Glu	Ile	Tyr	Gln	Thr	Lys
		355				360						365			
Leu	Gly	Pro	Asp	Asp	Pro	Asn	Val	Ala	Lys	Thr	Lys	Asn	Asn	Leu	Ala
	370					375					380				
Ser	Cys	Tyr	Leu	Lys	Gln	Gly	Lys	Phe	Lys	Gln	Ala	Glu	Thr	Leu	Tyr
385					390					395					400
Lys	Glu	Ile	Leu	Thr	Arg	Ala	His	Glu	Arg	Glu	Phe	Gly	Ser	Val	Asp
			405						410					415	
Asp	Glu	Asn	Lys	Pro	Ile	Trp	Met	His	Ala	Glu	Glu	Arg	Glu	Glu	Cys
			420					425					430		
Lys	Gly	Lys	Gln	Lys	Asp	Gly	Thr	Ser	Phe	Gly	Glu	Tyr	Gly	Gly	Trp
		435				440						445			
Tyr	Lys	Ala	Cys	Lys	Val	Asp	Ser	Pro	Thr	Val	Thr	Thr	Thr	Leu	Lys
	450					455						460			
Asn	Leu	Gly	Ala	Leu	Tyr	Arg	Arg	Gln	Gly	Lys	Phe	Glu	Ala	Ala	Glu
465					470					475					480
Thr	Leu	Glu	Glu	Ala	Ala	Met	Arg	Ser	Arg	Lys	Gln	Gly	Leu	Asp	Asn

				485					490					495			
Val	His	Lys	Gln	Arg	Val	Ala	Glu	Val	Leu	Asn	Asp	Pro	Glu	Asn	Met		
			500						505					510			
Glu	Lys	Arg	Arg	Ser	Arg	Glu	Ser	Leu	Asn	Val	Asp	Val	Val	Lys	Tyr		
		515						520					525				
Glu	Ser	Gly	Pro	Asp	Gly	Gly	Glu	Glu	Val	Ser	Met	Ser	Val	Glu	Trp		
	530					535					540						
Asn	Gly	Gly	Val	Ser	Gly	Arg	Ala	Ser	Phe	Cys	Gly	Lys	Arg	Gln	Gln		
545					550					555					560		
Gln	Gln	Trp	Pro	Gly	Arg	Arg	His	Arg									
				565													